

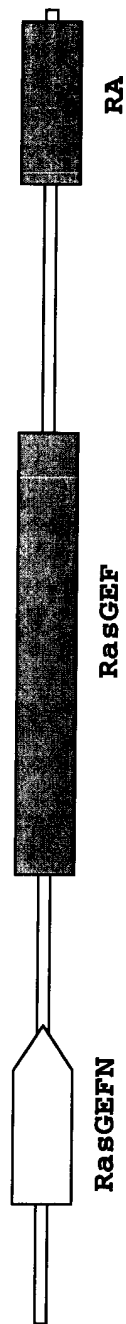


Annotated Sheet Showing Changes  
U.S. Application No.: 10/060,990  
Filing Date: January 30, 2002  
Y. Gu, et al. / PB0176  
Human RALGDS-Like Protein 3  
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# Structure of RGL3 and alignment of RasGEFN, RasGEF and RA motifs.

**FIG. 1A**  
RGL3 (710 a.a.)



~~FIG. 1~~



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**FIG. 1B**  
**RasGEFN motif**

	10	20	30	40	50	60
consensus	..... .....* .....* .....* .....* .....* .....*					
RGL3	1 CKGGLIKGGTLEKLIIEHLTEARDK-VDPTFVETFFLLTYRSFITTQELLQKLLRYNAIPP	59				
gi 1354501	64 SKVRVLRAARLERLVGELVFGDRE-QDPSEMPAFATYRTFVPTACLLGFLLP--PMPPP	120				
gi 158471	87 RSSRRLRAGTLEALVRHLLDARTAGADMFTPALLATHRAFTSTPALFGLVADRLEALES	146				
gi 544403	636 AGVPMIKGATLCKLIERLTYHIY--ADPTFVRTFLTYYFCSPQQLQLLVERFNIPDP	693				
	111 CKVRTVKAGTLEKLVEHLVPAFQg-SDLSYVTVFLCTYRAFTTTTQQQVLDLLFKRYGCILP	169				
	70	80	90	100	110	120
consensus	.....* .....* .....* .....* .....* .....* .....*					
RGL3	60 EGVE-----D-----IWVKEKVNPRRIQ---NRVLNILRLWV	88				
gi 1354501	121 PPPG-----V-----EIKKTAVQDLSFNknIRAVVSVLGSWL	152				
gi 158471	147 Y-----PPGELERTT---GVAISVLSTWL	167				
gi 544403	694 SLVYqdtgtagaggmgvggDkehknshredwkyRKYVQP--VQ---FRVLNVLRHWV	748				
	170 Yss-----eDg-----GPQDQLK---NAISSILGTWL	193				
	130	140	150	160		
consensus	.....* .....* .....* .....* .....* .....*					
RGL3	89 ENYWQDFEEDPKLNLFLFEE-FLELVDDK-KYPGLETSLQNILRRLS	132				
gi 1354501	153 QDHPQDFRDHPahsdlgsvrtflgwaapgsaeaqaekllfedflee	198				
gi 158471	168 ASHPEDFGSEVKGQLDRLE-SFLLRTGYaAREGVVGGsADLIRNLR	212				
gi 544403	749 DHHFYDFEKDPMLEKLLN-FLEHVNGK-SMRKWVDSVLKIVQRKN	792				
	194 DQYSEDFCQP-PDFPCLKQLVAYVQLNM-PGSDLERRAHLLLAQLE	237				

**FIG. 1**



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FIG. 1C

RasGEF motif

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consensus 1 LLLLDPKELAEQLTLLDFELFRKIDPSELLGSGVWGRSKKS--PSPL--NLERFIERFNE 56
RGL3      243 LLDPSVDEVAEQTLIDLELFKVRLYECLGSGVWQRDRPGaaGASP--TVRATVAQFNT 300
1BKD_S    171 LLTLHPHIEIARQLTLLSDLYRAVQPSLVGVTWKEDKEI--NSP--NLLKMIRHTTN 225
gi 544403 363 LLLFPPDLVAEQFTLMDAELFKKVVVPYHCLGSIWQRAKKG--KEHlapTIRATVAQFNN 420
gi 6919956 239 VLVFLADHLAEQLTLLDAELFLNLIPSCQLGGLGHRDRPG--HSHlcpSVRATVTQFNK 296

          70      80      90      100      110      120
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 57 VSNWVATEILKQTT-----P--KDAELLKFIQVAKHCRELNNFNSLMAI 100
RGL3      301 VTGCVLGSVLGAPG-----LaaPQARQLEKWIRIAQRCRELNRNFFSSLRAI 346
1BKD_S    226 LTLWFEEKIVETEN-----L--EERVAVVSRIIEILQVFQELNFFNGVLEV 269
gi 544403 421 VANCVITTCGLGDQSm-----ka--SDRARVVEHWIEVARECRVLKNFSSLYAI 466
gi 6919956 297 VAGAVVSSVLGATStgepggevtirpP--PQRARLLEKWIRVAEECRLLRNFFSSVYAV 354

          130      140      150      160      170      180
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 101 VSALSSSPIISRLKKTWEKLP SKYKKLFEELEELLDP SRNFKNYREALSSCN----- 151
RGL3      347 LSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEategsqeed 406
1BKD_S    270 VSAMNSSPVYRLDHTFEQIPSRQKKILEEAHELSE--DHYKKYLAKLR SIN----- 318
gi 544403 467 LSALQSNAIHRLKKTWEESVRGSRFVFQKLSEIFSDENNYSLSRELLIKEGtskfalem 526
gi 6919956 355 VSALQSSPIHRLRAAWGEATRDSLRVFSLLCQIFSeedNYSQSRELLVQEVklqsp leph 414

          190      200      210      220      230      240
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
consensus 152 -----LPPCIPFLGVLLKDLTFIDEGNPDFLKN---GLVNFKEKRRKIAKIL 194
RGL3      407 n-----tpgslpskppPGVPVYLGTFLTDLVMDLTALPDMLEG---DLINFEKRRKEWEIL 459
1BKD_S    319 -----PPCVPFPGIYLTNILKTEEGNPEVLKRhgkELINFSKRRKVAEIT 363
gi 544403 527 nprtrqrqketgviQGTVPYLGTFLTDLVMDLTAMKDYLG---RLINFEKRRKEFEVI 583
gi 6919956 415 s-----kkaprsrgsgGVVPYLGTFLTDLVMDLAASKDELEN---GYINFDKRRKKEFAVL 467
```

FIG. 1



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**FIG. 1C**  
**RasGEF motif**  
**(Continued)**

	250	260	270	280	290	
	..... .....*..... .....*..... .....*..... .....*					
consensus	195 REIRQLQS--QYNLRPNRSDIQSLQQS--LDSLPEEN---ELYELSLRIEPRV	242				SEQ ID NO: 59
RGL3	460 ARIQQLQRrcQSYTLSPHPILAAL--HA--QNQLTEEQ----SYRLSRVIEPPa	506				SEQ ID NO: 60
1BKD_S	364 GEIQYQN--QPYCLRVE--SDIKRFFENLpMGNSMEKEftdYLFNKSLIEPRN	415				SEQ ID NO: 61
gi 544403	584 AQIKLLQsacNNYSIVPE--EHFGAWFRAM---GRLSEA----ESYNLSCELEPPS	630				SEQ ID NO: 62
gi 6919956	468 SELRRLLQnecRGYNLQPD-HDIQRWLQG---LRPLTEA----QSHRVSCVEVEPPG	514				SEQ ID NO: 63

**FIG. 1D**  
**RA motif**

	10	20	30	40	50	60	
	..... .....*..... .....*..... .....*..... .....*.....						
consensus	1 DQGVLRVYFQDLKPGVAYKTIrVSSedTAPDVVQlALEKFRlDDEdPEEYALVEVLSGDK	60					
RGL3	613 earVIRVSiDNDH-GNLYRSiLLTSQDKAPSVRRALQKHNVQPWACDYQLFQVLPGDR	671					
1EF5_A	17 DTCiIRiSVEdn-NGNMYKSiMLTSQDKTPAViQRAMSKHNLESDPAEEYELVQViSEDK	75					
1RLF	4 DCRIiRVQMElgeDGSVYKSiLVTSQDKAPSViSRVLKKNRDSAVASEFELVQLLPGDR	63					
1LXD_A	15 DCCiIRVSLDVd-NGNMYKSiLVTSQDKAPTViRKAMDKHNLDDEdPEYELLQIiSEdH	73					

	70	80	90	
	..... .....*..... .....*..... ...			
consensus	61 ERKLpDDENPLQLRLNLPRDGLSLRFLlKRrD	92	SEQ ID NO: 64	
RGL3	672 VLLiPDNANVFYAM----SPVAPRDFMLRRKE	699	SEQ ID NO: 65	
1EF5_A	76 ELViPDSANVFYAMNSQVN----FDFiLRKKN	103	SEQ ID NO: 66	
1RLF	64 ELTiPHSANVFYAMDGAS-----HDFiLRQRr	90	SEQ ID NO: 67	
1LXD_A	74 KLKiPENANVFYAMNSAAN-----YDFiLKRr-	100	SEQ ID NO: 68	

**FIG. 1**



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**Structure of RGL3 and alignment of RasGEFN,  
RasGEF and RA motifs.**

**FIG. 1A**  
**RGL3 (710 a.a.)**





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**FIG. 1B**  
**RasGEFN motif**

	10	20	30	40	50	60
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	1 CKGGLIKGGTLEKLIIEHLTEARDK-VDPFTFVEITFLLTYSFITTQELLQKLLYRYNAIPP	59				
gi 1354501	64 SKVRVLRAARLERLVGELVFGDRE-QDPSPMPAFATYRTFVPTACLLGFLLP--PMPPP	120				
gi 158471	87 RSSRRLRAGTLEALVRHLLDARTAGADMFTPALLATHRAFTSTPALFGLVADRLEALES	146				
gi 544403	636 AGVPMIKGATLCKLIERLTYHIY--ADPTFVRTFLTTRYFCSPQQLQLLVERFNIPDP	693				
	111 CKVRTVKAGTLEKLVHLPVAFQg-SDLSYVTVFLCTYRAFTTTTQQVLDLLFKRYGCILP	169				
	70	80	90	100	110	120
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	60 EGVE-----D-----D-----IWVKEKVNPRRIQ---NRVLNILRLWV	88				
gi 1354501	121 PPPG-----V-----EIKKTAVQDLSFNknlRAVSVLGSWL	152				
gi 158471	147 Y-----PPGELERTT---GVAISVLSTWL	167				
gi 544403	694 SLVYqdtgtagagmgvggDkehknshredwkRYRKEYVQP--VQ---FRVLNVLRHVV	748				
	170 Yss-----eDg-----GPQDQLK---NAISSILGTWL	193				
	130	140	150	160		
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	89 ENYWQDFEEDPKLNLFLFEE-FLELVDDK-KYPGLETSLQNILRLRLS	132				
gi 1354501	153 QDHPQDFRDHPahsdlgsvrtflgwaapgsaeaklledflee	198				
gi 158471	168 ASHPEDFGSEVKGQLDRLE-SFLLRGTGYaAREGVVGGsADLIRNLR	212				
gi 544403	749 DHHFYDFEKDPMLEKLLN-FLEHVNGK-SMRKWVDSVLKIVQRKN	792				
	194 DQYSEDFCQP-PDFPCLKQLVAYVQLNM-PGSDLERRAHLLLAQLE	237				



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**FIG. 1C**  
**RasGEF motif**

	10	20	30	40	50	60
consensus	1	LLLLDPKELAEQLTLDDFELFRKIDPSELLG	SVWGKR	SKKS--PSPL--NLERFIERFNE	56	
RGL3	243	LLDFSDEVAEQTLTIDLELFSKVRLYECLG	SVWSQR	DRPGaaGASP--TVRATVAQFNT	300	
1BKD_S	171	LLTLHPIEIARQLTLLLESDLYRAVQPS	ELVGSV	WTKEIKEI--NSP--NLLKMIRHTTN	225	
gi 544403	363	LLLFPDDLVAEQFTLMDAELFKKVVYPYH	CLGSIW	SQRAKKG--KEHlapTIRATVAQFNN	420	
gi 6919956	239	VLVFLADHLAEQLTLDDAELFLNLIPSQ	CLGGLW	GHDRPG--HSHLcpSVRATVTQFNK	296	
	70	80	90	100	110	120
consensus	57	VSNWVATEILKQTT-----P--KDR	AELL	SKFIQVAKHCRELNFNNSLMAI	100	
RGL3	301	VTGCVLGSLGAPG-----LaaPQ	RAQR	LEKWIRIAQRCRELRNFSSLRAI	346	
1BKD_S	226	LTLWFEKCIIVETEN-----L--E	ERVAV	VSRIIEILQVFQELNNGVLEV	269	
gi 544403	421	VANCVITTCLDGQSm-----ka--	SDR	RVVEHWIEVARECRVLKNFSSLYAI	466	
gi 6919956	297	VAGAVVSSVLGATStgepggevtirp	rP--PQ	RARLLEKWIRVAEECRLLRNFSSVYAV	354	
	130	140	150	160	170	180
consensus	101	VSALSSSPIRLKKTWEKLPSKYKKL	FEEL	LELLDPSRNFKNYREALSSCN-----	151	
RGL3	347	LSALQSNPIYRLKRSWGA	VSREPL	STFRKLSQIFSDENNHLSSREILFQEEategsqeed	406	
1BKD_S	270	VSAMNSSPVYRLDHTFEQIPSRQKK	ILEEA	HELSE--DHYKKYLAKLRSIN-----	318	
gi 544403	467	LSALQSNAIHRLKKTWEEVSRG	SFRVFQ	KLSEIFsdenNYSLSRELLIKEGtskfatem	526	
gi 6919956	355	VSALQSSPIHRLRAAWGEATR	SLRVF	SSLQCIFseedNYSQSRELLVQEVklqsplep	414	
	190	200	210	220	230	240
consensus	152	-----LPPCIPFLGVLLKDLT	FIDE	GNPDFLKN--GLVNF	EKKRRIA	KIL 194
RGL3	407	n-----tpgslpskpp	PGVPY	LGTFLTDLVMLDTALPDMLEG---	DLIN	EKKRKEWEIL 459
1BKD_S	319	-----PPCVPFFGIYLT	NILK	TEEGNPEVLKRhgkelINFSKRRKVAEIT	363	
gi 544403	527	nprrtqrrqketgviQGTVPY	LGTFL	TDLVMLDTAMKDYLYG---RLIN	EKKRKEFEVI 583	
gi 6919956	415	s-----kkaprsrg	GGVVPY	LGTFLKDLVMLDAASKDELEN---GYIN	FDKRRKEFAVL 467	



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## FIG. 1C

### RasGEF motif

(Continued)

	250	260	270	280	290	
	.....*	.....*	.....*	.....*	.....*	
consensus	195	REIRQLQS--QPYNLRPNRSDIQSL	LLQQS--LDSLPEEN---	ELYELSLRIEPRV	242	SEQ ID NO: 59
RGL3	460	ARIQQLQRrcQSYTLSPHPILAAL--	HA--QNQLTEEQ----	SYRLSRVIEPPa	506	SEQ ID NO: 60
1BKD_S	364	GEIQQYQN--QPYCLRVE-SDIKRFFENL	mpMGNSMEKEftdYLFNKSL	EIEPRN	415	SEQ ID NO: 61
gi 544403	584	AQIKLLQSacNNYSIVPE-EHFGAWFRAM---	GRLSEA----	ESYNLSCELEPPS	630	SEQ ID NO: 62
gi 6919956	468	SELRRQLNecRGYNLQPD-HDIQRWLQG---	LRPLTEA----	QSHRVSCVEVEPPG	514	SEQ ID NO: 63

## FIG. 1D

### RA motif

	10	20	30	40	50	60
	.....*	.....*	.....*	.....*	.....*	.....*
consensus	1	DQGVLRVYFQDLKPGVAYKTI	RVSSSEDPDVVQLALEKFR	LDDEDP	EEYALVEVLSGDK	60
RGL3	613	earVIRVSI	DNDH-GNLYRSIL	LTSDQKAPSVVRRALQKHNV	PQFWACDYQLFQVLP	671
1EF5_A	17	DTCIIRISVEDn-NGNMYKS	IMLTSDQKTPAVIQRAMSKHN	LES	SDPAEEYELVQVISEDK	75
1RLF	4	DCRIIRVQMElgeDGSVYKS	ILVTSQDKAPSVISRVLKKNR	DSAVASEFELVQLLP	63	
1LXD_A	15	DCCIIRVSLDvd-NGNMYKS	ILVTSQDKAPT	VIRKAMDKHNLDEDEPEDYELLQII	ISEDH	73

	70	80	90		
	.....*	.....*	.....*	.....*	
consensus	61	ERKLPDDENPLQLRLNLP	RDGLSLRFL	KKRD 92	SEQ ID NO: 64
RGL3	672	VLLIPDNANVFYAM----	SPVAPRDFMLRRKE	699	SEQ ID NO: 65
1EF5_A	76	ELVIPDSANVFYAMNSQVN----	FDFILRKKN	103	SEQ ID NO: 66
1RLF	64	ELTIPHSANVFYAMDGAS-----	HDFLLRQRR	90	SEQ ID NO: 67
1LXD_A	74	KLKIPENANVFYAMNSAAN----	YDFILKKR-	100	SEQ ID NO: 68